



SeqListing.txt
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lemischka, Ihor R.

(ii) TITLE OF INVENTION: METHOD FOR ISOLATING CELLS EXPRESSING
FLK-2 RECEPTORS AND ISOLATED POPULATIONS
OF CELLS THAT EXPRESS FLK-2 RECEPTORS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Kenyon & Kenyon
(B) STREET: One Broadway
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/919,408
(B) FILING DATE: 31-JUL-2001

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/208,786
(B) FILING DATE: 10-DEC-1998

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/021,324
(B) FILING DATE: 10-FEB-1998

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/601,891
(B) FILING DATE: 15-FEB-1996

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/252,498
(B) FILING DATE: 31-OCT-1994

(vii) PRIOR APPLICATION DATA:

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- (A) APPLICATION NUMBER: US 08/055,269
- (B) FILING DATE: 30-APR-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/977,451
- (B) FILING DATE: 19-NOV-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/975,049
- (B) FILING DATE: 12-NOV-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/906,397
- (B) FILING DATE: 26-JUN-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/813,593
- (B) FILING DATE: 24-DEC-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/793,065
- (B) FILING DATE: 15-NOV-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/728,913
- (B) FILING DATE: 28-JUN-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/679,666
- (B) FILING DATE: 02-APR-1991

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Wieckowski, Elizabeth M.
- (B) REGISTRATION NUMBER: 42,226
- (C) REFERENCE/DOCKET NUMBER: 11245/46115

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212-425-7200
- (B) TELEFAX: 212-425-5288

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 112..3006

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 31..111

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 31..3009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCCTGGC TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC
54

Met Arg Ala Leu Ala Gln Arg Ser
-27 -25 -20

GAC CGG CGG CTG CTG CTG CTT GTT GTT TTG TCA GTA ATG ATT CTT GAG
102

Asp Arg Arg Leu Leu Leu Leu Val Val Leu Ser Val Met Ile Leu Glu
-15 -10 -5

ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT
150

Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser
1 5 10

CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG
198

His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met
15 20 25

GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT
246

Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser

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30		35		40		45
GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG						
294						
Glu Gly Thr Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly						
		50		55		60
TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC						
342						
Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys						
		65		70		75
CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT						
390						
Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp						
		80		85		90
TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG						
438						
Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu						
		95		100		105
ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC						
486						
Thr Gln Ala Gly Glu Tyr Leu Leu His Ile Gln Ser Glu Arg Ala Asn						
		110		115		125
TAC ACA GTA CTG TTC ACA GTG AAT GTA AGA GAT ACA CAG CTG TAT GTG						
534						
Tyr Thr Val Leu Phe Thr Val Asn Val Arg Asp Thr Gln Leu Tyr Val						
		130		135		140
CTA AGG AGA CCT TAC TTT AGG AAG ATG GAA AAC CAG GAT GCA CTG CTC						
582						
Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu						
		145		150		155
TGC ATC TCC GAG GGT GTT CCG GAG CCC ACT GTG GAG TGG GTG CTC TGC						
630						
Cys Ile Ser Glu Gly Val Pro Glu Pro Thr Val Glu Trp Val Leu Cys						
		160		165		170
AGC TCC CAC AGG GAA AGC TGT AAA GAA GAA GGC CCT GCT GTT GTC AGA						
678						
Ser Ser His Arg Glu Ser Cys Lys Glu Glu Gly Pro Ala Val Val Arg						
		175		180		185
AAG GAG GAA AAG GTA CTT CAT GAG TTG TTC GGA ACA GAC ATC AGA TGC						

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726	Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	
190						195					200					205	
TGT	GCT	AGA	AAT	GCA	CTG	GGC	CGC	GAA	TGC	ACC	AAG	CTG	TTC	ACC	ATA		
774	Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg	Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	
				210						215					220		
GAT	CTA	AAC	CAG	GCT	CCT	CAG	AGC	ACA	CTG	CCC	CAG	TTA	TTC	CTG	AAA		
822	Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser	Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	
			225					230						235			
GTG	GGG	GAA	CCC	TTG	TGG	ATC	AGG	TGT	AAG	GCC	ATC	CAT	GTG	AAC	CAT		
870	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys	Lys	Ala	Ile	His	Val	Asn	His	
		240					245						250				
GGA	TTC	GGG	CTC	ACC	TGG	GAG	CTG	GAA	GAC	AAA	GCC	CTG	GAG	GAG	GGC		
918	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	
	255						260					265					
AGC	TAC	TTT	GAG	ATG	AGT	ACC	TAC	TCC	ACA	AAC	AGG	ACC	ATG	ATT	CGG		
966	Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	
270						275					280					285	
ATT	CTC	TTG	GCC	TTT	GTG	TCT	TCC	GTG	GGA	AGG	AAC	GAC	ACC	GGA	TAT	1	
014	Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser	Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	
				290						295					300		
TAC	ACC	TGC	TCT	TCC	TCA	AAG	CAC	CCC	AGC	CAG	TCA	GCG	TTG	GTG	ACC	1	
062	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	
			305						310					315			
ATC	CTA	GAA	AAA	GGG	TTT	ATA	AAC	GCT	ACC	AGC	TCG	CAA	GAA	GAG	TAT	1	
110	Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn	Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	
		320						325					330				
GAA	ATT	GAC	CCG	TAC	GAA	AAG	TTC	TGC	TTC	TCA	GTC	AGG	TTT	AAA	GCG	1	
158	Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe	Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	
	335						340					345					

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TAC	CCA	CGA	ATC	CGA	TGC	ACG	TGG	ATC	TTC	TCT	CAA	GCC	TCA	TTT	CCT	1
206																
Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp	Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	
350					355					360					365	
TGT	GAA	CAG	AGA	GGC	CTG	GAG	GAT	GGG	TAC	AGC	ATA	TCT	AAA	TTT	TGC	1
254																
Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	
				370					375					380		
GAT	CAT	AAG	AAC	AAG	CCA	GGA	GAG	TAC	ATA	TTC	TAT	GCA	GAA	AAT	GAT	1
302																
Asp	His	Lys	Asn	Lys	Pro	Gly	Glu	Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	
			385					390					395			
GAC	GCC	CAG	TTC	ACC	AAA	ATG	TTC	ACG	CTG	AAT	ATA	AGA	AAG	AAA	CCT	1
350																
Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	
		400					405					410				
CAA	GTG	CTA	GCA	AAT	GCC	TCA	GCC	AGC	CAG	GCG	TCC	TGT	TCC	TCT	GAT	1
398																
Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala	Ser	Gln	Ala	Ser	Cys	Ser	Ser	Asp	
	415					420					425					
GGC	TAC	CCG	CTA	CCC	TCT	TGG	ACC	TGG	AAG	AAG	TGT	TCG	GAC	AAA	TCT	1
446																
Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	Lys	Lys	Cys	Ser	Asp	Lys	Ser	
430					435					440					445	
CCC	AAT	TGC	ACG	GAG	GAA	ATC	CCA	GAA	GGA	GTT	TGG	AAT	AAA	AAG	GCT	1
494																
Pro	Asn	Cys	Thr	Glu	Glu	Ile	Pro	Glu	Gly	Val	Trp	Asn	Lys	Lys	Ala	
				450					455					460		
AAC	AGA	AAA	GTG	TTT	GGC	CAG	TGG	GTG	TCG	AGC	AGT	ACT	CTA	AAT	ATG	1
542																
Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	Ser	Ser	Ser	Thr	Leu	Asn	Met	
			465					470					475			
AGT	GAG	GCC	GGG	AAA	GGG	CTT	CTG	GTC	AAA	TGC	TGT	GCG	TAC	AAT	TCT	1
590																
Ser	Glu	Ala	Gly	Lys	Gly	Leu	Leu	Val	Lys	Cys	Cys	Ala	Tyr	Asn	Ser	
		480					485					490				
ATG	GGC	ACG	TCT	TGC	GAA	ACC	ATC	TTT	TTA	AAC	TCA	CCA	GGC	CCC	TTC	1
638																

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Met	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Phe	Leu	Asn	Ser	Pro	Gly	Pro	Phe	
495						500					505					
CCT 686	TTC	ATC	CAA	GAC	AAC	ATC	TCC	TTC	TAT	GCG	ACC	ATT	GGG	CTC	TGT	1
Pro 510	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	Tyr	Ala	Thr	Ile	Gly	Leu	Cys	
					515					520					525	
CTC 734	CCC	TTC	ATT	GTT	GTT	CTC	ATT	GTG	TTG	ATC	TGC	CAC	AAA	TAC	AAA	1
Leu	Pro	Phe	Ile	Val	Val	Leu	Ile	Val	Leu	Ile	Cys	His	Lys	Tyr	Lys	
				530					535					540		
AAG 782	CAA	TTT	AGG	TAC	GAG	AGT	CAG	CTG	CAG	ATG	ATC	CAG	GTG	ACT	GGC	1
Lys	Gln	Phe	Arg	Tyr	Glu	Ser	Gln	Leu	Gln	Met	Ile	Gln	Val	Thr	Gly	
			545					550					555			
CCC 830	CTG	GAT	AAC	GAG	TAC	TTC	TAC	GTT	GAC	TTC	AGG	GAC	TAT	GAA	TAT	1
Pro	Leu	Asp	Asn	Glu	Tyr	Phe	Tyr	Val	Asp	Phe	Arg	Asp	Tyr	Glu	Tyr	
		560					565					570				
GAC 878	CTT	AAG	TGG	GAG	TTC	CCG	AGA	GAG	AAC	TTA	GAG	TTT	GGG	AAG	GTC	1
Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	Glu	Asn	Leu	Glu	Phe	Gly	Lys	Val	
		575				580					585					
CTG 926	GGG	TCT	GGC	GCT	TTC	GGG	AGG	GTG	ATG	AAC	GCC	ACG	GCC	TAT	GGC	1
Leu	Gly	Ser	Gly	Ala	Phe	Gly	Arg	Val	Met	Asn	Ala	Thr	Ala	Tyr	Gly	
590				595						600				605		
ATT 974	AGT	AAA	ACG	GGA	GTC	TCA	ATT	CAG	GTG	GCG	GTG	AAG	ATG	CTA	AAA	1
Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln	Val	Ala	Val	Lys	Met	Leu	Lys	
				610				615						620		
GAG 022	AAA	GCT	GAC	AGC	TGT	GAA	AAA	GAA	GCT	CTC	ATG	TCG	GAG	CTC	AAA	2
Glu	Lys	Ala	Asp	Ser	Cys	Glu	Lys	Glu	Ala	Leu	Met	Ser	Glu	Leu	Lys	
			625					630					635			
ATG 070	ATG	ACC	CAC	CTG	GGA	CAC	CAT	GAC	AAC	ATC	GTG	AAT	CTG	CTG	GGG	2
Met	Met	Thr	His	Leu	Gly	His	His	Asp	Asn	Ile	Val	Asn	Leu	Leu	Gly	
		640					645					650				

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GCA	TGC	ACA	CTG	TCA	GGG	CCA	GTG	TAC	TTG	ATT	TTT	GAA	TAT	TGT	TGC	2
118																
Ala	Cys	Thr	Leu	Ser	Gly	Pro	Val	Tyr	Leu	Ile	Phe	Glu	Tyr	Cys	Cys	
655						660					665					
TAT	GGT	GAC	CTC	CTC	AAC	TAC	CTA	AGA	AGT	AAA	AGA	GAG	AAG	TTT	CAC	2
166																
Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	Ser	Lys	Arg	Glu	Lys	Phe	His	
670					675					680					685	
AGG	ACA	TGG	ACA	GAG	ATT	TTT	AAG	GAA	CAT	AAT	TTC	AGT	TCT	TAC	CCT	2
214																
Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	Glu	His	Asn	Phe	Ser	Ser	Tyr	Pro	
				690					695					700		
ACT	TTC	CAG	GCA	CAT	TCA	AAT	TCC	AGC	ATG	CCT	GGT	TCA	CGA	GAA	GTT	2
262																
Thr	Phe	Gln	Ala	His	Ser	Asn	Ser	Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	
			705						710					715		
CAG	TTA	CAC	CCG	CCC	TTG	GAT	CAG	CTC	TCA	GGG	TTC	AAT	GGG	AAT	TCA	2
310																
Gln	Leu	His	Pro	Pro	Leu	Asp	Gln	Leu	Ser	Gly	Phe	Asn	Gly	Asn	Ser	
		720					725					730				
ATT	CAT	TCT	GAA	GAT	GAG	ATT	GAA	TAT	GAA	AAC	CAG	AAG	AGG	CTG	GCA	2
358																
Ile	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	Glu	Asn	Gln	Lys	Arg	Leu	Ala	
	735					740					745					
GAA	GAA	GAG	GAG	GAA	GAT	TTG	AAC	GTG	CTG	ACG	TTT	GAA	GAC	CTC	CTT	2
406																
Glu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	Phe	Glu	Asp	Leu	Leu	
750					755					760					765	
TGC	TTT	GCG	TAC	CAA	GTG	GCC	AAA	GGC	ATG	GAA	TTC	CTG	GAG	TTC	AAG	2
454																
Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Glu	Phe	Lys	
				770					775					780		
TCG	TGT	GTC	CAC	AGA	GAC	CTG	GCA	GCC	AGG	AAT	GTG	TTG	GTC	ACC	CAC	2
502																
Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	His	
			785					790					795			
GGG	AAG	GTG	GTG	AAG	ATC	TGT	GAC	TTT	GGA	CTG	GCC	CGA	GAC	ATC	CTG	2
550																
Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Leu	

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805

800		810	
AGC 598	GAC TCC AGC TAC GTC GTC AGG GGC AAC GCA CGG CTG CCG GTG AAG		2
Ser 815	Asp Ser Ser Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys		
		820 825	
TGG 646	ATG GCA CCC GAG AGC TTA TTT GAA GGG ATC TAC ACA ATC AAG AGT		2
Trp 830	Met Ala Pro Glu Ser Leu Phe Glu Gly Ile Tyr Thr Ile Lys Ser		
		835 840 845	
GAC 694	GTC TGG TCC TAC GGC ATC CTT CTC TGG GAG ATA TTT TCA CTG GGT		2
Asp	Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly		
		850 855 860	
GTG 742	AAC CCT TAC CCT GGC ATT CCT GTC GAC GCT AAC TTC TAT AAA CTG		2
Val	Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala Asn Phe Tyr Lys Leu		
		865 870 875	
ATT 790	CAG AGT GGA TTT AAA ATG GAG CAG CCA TTC TAT GCC ACA GAA GGG		2
Ile	Gln Ser Gly Phe Lys Met Glu Gln Pro Phe Tyr Ala Thr Glu Gly		
		880 885 890	
ATA 838	TAC TTT GTA ATG CAA TCC TGC TGG GCT TTT GAC TCA AGG AAG CGG		2
Ile	Tyr Phe Val Met Gln Ser Cys Trp Ala Phe Asp Ser Arg Lys Arg		
		895 900 905	
CCA 886	TCC TTC CCC AAC CTG ACT TCA TTT TTA GGA TGT CAG CTG GCA GAG		2
Pro 910	Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly Cys Gln Leu Ala Glu		
		915 920 925	
GCA 934	GAA GAA GCA TGT ATC AGA ACA TCC ATC CAT CTA CCA AAA CAG GCG		2
Ala	Glu Glu Ala Cys Ile Arg Thr Ser Ile His Leu Pro Lys Gln Ala		
		930 935 940	
GCC 982	CCT CAG CAG AGA GGC GGG CTC AGA GCC CAG TCG CCA CAG CGC CAG		2
Ala	Pro Gln Gln Arg Gly Gly Leu Arg Ala Gln Ser Pro Gln Arg Gln		
		945 950 955	
GTG	AAG ATT CAC AGA GAA AGA AGT TAGCGAGGAG GCCTTGGACC CCGCCACCCT		3

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Val Lys Ile His Arg Glu Arg Ser
 960 965

AGCAGGCTGT AGACCGCAGA GCCAAGATTA GCCTCGCCTC TGAGGAAGCG CCCTACAGCG 3
 096

CGTTGCTTCG CTGGACTTTT CTCTAGATGC TGTCTGCCAT TACTCCAAAG TGA CTTCTAT 3
 156

AAAATCAAAC CTCTCCTCGC ACAGGCGGGA GAGCCAATAA TGAGACTTGT TGGTGAGCCC 3
 216

GCCTACCCTG GGGGCCTTTC CACGAGCTTG AGGGGAAAGC CATGTATCTG AAATATAGTA 3
 276

TATTCTTGTA AATACGTGAA ACAAACCAAA CCCGTTTTTTT GCTAAGGGAA AGCTAAATAT 3
 336

GATTTTAAA AATCTATGTT TTAAATACT ATGTAAC TTTTTCATCTATT TAGTGATATA 3
 396

TTTTATGGAT GGAAATAAAC TTTCTACTGT AAAAAAAAAA AAAAAAAAAA AAAAAAA 3
 453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ala Leu Ala Gln Arg Ser Asp Arg Arg Leu Leu Leu Leu Val
 -27 -25 -20 -15

Val Leu Ser Val Met Ile Leu Glu Thr Val Thr Asn Gln Asp Leu Pro
 -10 -5 1 5

Val Ile Lys Cys Val Leu Ile Ser His Glu Asn Asn Gly Ser Ser Ala
 10 15 20

Gly Lys Pro Ser Ser Tyr Arg Met Val Arg Gly Ser Pro Glu Asp Leu
 25 30 35

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Gln	Cys	Thr	Pro	Arg	Arg	Gln	Ser	Glu	Gly	Thr	Val	Tyr	Glu	Ala	Ala		
		40					45					50					
Thr	Val	Glu	Val	Ala	Glu	Ser	Gly	Ser	Ile	Thr	Leu	Gln	Val	Gln	Leu		
	55					60					65						
Ala	Thr	Pro	Gly	Asp	Leu	Ser	Cys	Leu	Trp	Val	Phe	Lys	His	Ser	Ser		
70					75					80					85		
Leu	Gly	Cys	Gln	Pro	His	Phe	Asp	Leu	Gln	Asn	Arg	Gly	Ile	Val	Ser		
				90					95					100			
Met	Ala	Ile	Leu	Asn	Val	Thr	Glu	Thr	Gln	Ala	Gly	Glu	Tyr	Leu	Leu		
			105					110					115				
His	Ile	Gln	Ser	Glu	Arg	Ala	Asn	Tyr	Thr	Val	Leu	Phe	Thr	Val	Asn		
		120					125					130					
Val	Arg	Asp	Thr	Gln	Leu	Tyr	Val	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys		
	135					140					145						
Met	Glu	Asn	Gln	Asp	Ala	Leu	Leu	Cys	Ile	Ser	Glu	Gly	Val	Pro	Glu		
150					155					160					165		
Pro	Thr	Val	Glu	Trp	Val	Leu	Cys	Ser	Ser	His	Arg	Glu	Ser	Cys	Lys		
				170					175					180			
Glu	Glu	Gly	Pro	Ala	Val	Val	Arg	Lys	Glu	Glu	Lys	Val	Leu	His	Glu		
			185					190					195				
Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg		
		200					205					210					
Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser		
	215					220					225						
Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg		
230					235					240					245		
Cys	Lys	Ala	Ile	His	Val	Asn	His	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu		
				250					255					260			
Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr		
			265					270					275				
Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser		
		280					285					290					

SeqListing.txt

Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His
	295					300					305				
Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn
310					315					320					325
Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe
				330					335					340	
Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp
			345					350					355		
Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp
		360					365					370			
Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	Asp	His	Lys	Asn	Lys	Pro	Gly	Glu
	375					380					385				
Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe
390					395					400					405
Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala
				410					415					420	
Ser	Gln	Ala	Ser	Cys	Ser	Ser	Asp	Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr
			425					430					435		
Trp	Lys	Lys	Cys	Ser	Asp	Lys	Ser	Pro	Asn	Cys	Thr	Glu	Glu	Ile	Pro
		440					445					450			
Glu	Gly	Val	Trp	Asn	Lys	Lys	Ala	Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp
	455					460					465				
Val	Ser	Ser	Ser	Thr	Leu	Asn	Met	Ser	Glu	Ala	Gly	Lys	Gly	Leu	Leu
470					475					480					485
Val	Lys	Cys	Cys	Ala	Tyr	Asn	Ser	Met	Gly	Thr	Ser	Cys	Glu	Thr	Ile
				490					495					500	
Phe	Leu	Asn	Ser	Pro	Gly	Pro	Phe	Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser
			505					510					515		
Phe	Tyr	Ala	Thr	Ile	Gly	Leu	Cys	Leu	Pro	Phe	Ile	Val	Val	Leu	Ile
		520					525					530			
Val	Leu	Ile	Cys	His	Lys	Tyr	Lys	Lys	Gln	Phe	Arg	Tyr	Glu	Ser	Gln
	535					540					545				

SeqListing.txt

Leu	Gln	Met	Ile	Gln	Val	Thr	Gly	Pro	Leu	Asp	Asn	Glu	Tyr	Phe	Tyr	550	555	560	565
Val	Asp	Phe	Arg	Asp	Tyr	Glu	Tyr	Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	570	575	580	
Glu	Asn	Leu	Glu	Phe	Gly	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Arg	585	590	595	
Val	Met	Asn	Ala	Thr	Ala	Tyr	Gly	Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	600	605	610	
Gln	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Lys	Ala	Asp	Ser	Cys	Glu	Lys	615	620	625	
Glu	Ala	Leu	Met	Ser	Glu	Leu	Lys	Met	Met	Thr	His	Leu	Gly	His	His	630	635	640	645
Asp	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Leu	Ser	Gly	Pro	Val	650	655	660	
Tyr	Leu	Ile	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	665	670	675	
Arg	Ser	Lys	Arg	Glu	Lys	Phe	His	Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	680	685	690	
Glu	His	Asn	Phe	Ser	Ser	Tyr	Pro	Thr	Phe	Gln	Ala	His	Ser	Asn	Ser	695	700	705	
Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	Gln	Leu	His	Pro	Pro	Leu	Asp	Gln	710	715	720	725
Leu	Ser	Gly	Phe	Asn	Gly	Asn	Ser	Ile	His	Ser	Glu	Asp	Glu	Ile	Glu	730	735	740	
Tyr	Glu	Asn	Gln	Lys	Arg	Leu	Ala	Glu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	745	750	755	
Val	Leu	Thr	Phe	Glu	Asp	Leu	Leu	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	760	765	770	
Gly	Met	Glu	Phe	Leu	Glu	Phe	Lys	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	775	780	785	
Ala	Arg	Asn	Val	Leu	Val	Thr	His	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	790	795	800	805

SeqListing.txt

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Phe Gly Leu Ala Arg Asp Ile Leu Ser Asp Ser Ser Tyr Val Val Arg
      810      815      820
Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe
      825      830      835
Glu Gly Ile Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu
      840      845      850
Leu Trp Glu Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro
      855      860      865
Val Asp Ala Asn Phe Tyr Lys Leu Ile Gln Ser Gly Phe Lys Met Glu
      870      875      880      885
Gln Pro Phe Tyr Ala Thr Glu Gly Ile Tyr Phe Val Met Gln Ser Cys
      890      895      900
Trp Ala Phe Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser
      905      910      915
Phe Leu Gly Cys Gln Leu Ala Glu Ala Glu Glu Ala Cys Ile Arg Thr
      920      925      930
Ser Ile His Leu Pro Lys Gln Ala Ala Pro Gln Gln Arg Gly Gly Leu
      935      940      945
Arg Ala Gln Ser Pro Gln Arg Gln Val Lys Ile His Arg Glu Arg Ser
      950      955      960      965

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SeqListing.txt

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 58..3039

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 139..3036

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 58..138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGGCGGCA TCCGAGGGCT GGGCCGGCGC CCTGGGGGAC CCCGGGCTCC GGAGGCC
57

ATG CCG GCG TTG GCG CGC GAC GCG GGC ACC GTG CCG CTG CTC GTT GTT
105

Met Pro Ala Leu Ala Arg Asp Ala Gly Thr Val Pro Leu Leu Val Val
-27 -25 -20 -15

TTT TCT GCA ATG ATA TTT GGG ACT ATT ACA AAT CAA GAT CTG CCT GTG
153

Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val
-10 -5 1 5

ATC AAG TGT GTT TTA ATC AAT CAT AAG AAC AAT GAT TCA TCA GTG GGG
201

Ile Lys Cys Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly
10 15 20

AAG TCA TCA TCA TAT CCC ATG GTA TCA GAA TCC CCG GAA GAC CTC GGG
249

Lys Ser Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly
25 30 35

TGT GCG TTG AGA CCC CAG AGC TCA GGG ACA GTG TAC GAA GCT GCC GCT
297

Cys Ala Leu Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala
40 45 50

GTG GAA GTG GAT GTA TCT GCT TCC ATC ACA CTG CAA GTG CTG GTC GAT

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345

Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp
55 60 65

GCC CCA GGG AAC ATT TCC TGT CTC TGG GTC TTT AAG CAC AGC TCC CTG
393

Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu
70 75 80 85

AAT TGC CAG CCA CAT TTT GAT TTA CAA AAC AGA GGA GTT GTT TCC ATG
441

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
90 95 100

GTC ATT TTG AAA ATG ACA GAA ACC CAA GCT GGA GAA TAC CTA CTT TTT
489

Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
105 110 115

ATT CAG AGT GAA GCT ACC AAT TAC ACA ATA TTG TTT ACA GTG AGT ATA
537

Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
120 125 130

AGA AAT ACC CTG CTT TAC ACA TTA AGA AGA CCT TAC TTT AGA AAA ATG
585

Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
135 140 145

GAA AAC CAG GAC GCC CTG GTC TGC ATA TCT GAG AGC GTT CCA GAG CCG
633

Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
150 155 160 165

ATC GTG GAA TGG GTG CTT TGC GAT TCA CAG GGG GAA AGC TGT AAA GAA
681

Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
170 175 180

GAA AGT CCA GCT GTT GTT AAA AAG GAG GAA AAA GTG CTT CAT GAA TTA
729

Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
185 190 195

TTT GGG ACG GAC ATA AGG TGC TGT GCC AGA AAT GAA CTG GGC AGG GAA
777

Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
200 205 210

SeqListing.txt

TGC	ACC	AGG	CTG	TTC	ACA	ATA	GAT	CTA	AAT	CAA	ACT	CCT	CAG	ACC	ACA		
825																	
Cys	Thr	Arg	Leu	Phe	Thr	Ile	Asp	Leu	Asn	Gln	Thr	Pro	Gln	Thr	Thr		
	215					220					225						
TTG	CCA	CAA	TTA	TTT	CTT	AAA	GTA	GGG	GAA	CCC	TTA	TGG	ATA	AGG	TGC		
873																	
Leu	Pro	Gln	Leu	Phe	Leu	Lys	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys		
230					235					240					245		
AAA	GCT	GTT	CAT	GTG	AAC	CAT	GGA	TTC	GGG	CTC	ACC	TGG	GAA	TTA	GAA		
921																	
Lys	Ala	Val	His	Val	Asn	His	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu		
			250						255					260			
AAC	AAA	GCA	CTC	GAG	GAG	GGC	AAC	TAC	TTT	GAG	ATG	AGT	ACC	TAT	TCA		
969																	
Asn	Lys	Ala	Leu	Glu	Glu	Gly	Asn	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser		
		265						270					275				
ACA	AAC	AGA	ACT	ATG	ATA	CGG	ATT	CTG	TTT	GCT	TTT	GTA	TCA	TCA	GTG		1
017																	
Thr	Asn	Arg	Thr	Met	Ile	Arg	Ile	Leu	Phe	Ala	Phe	Val	Ser	Ser	Val		
		280					285					290					
GCA	AGA	AAC	GAC	ACC	GGA	TAC	TAC	ACT	TGT	TCC	TCT	TCA	AAG	CAT	CCC		1
065																	
Ala	Arg	Asn	Asp	Thr	Gly	Tyr	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro		
	295					300					305						
AGT	CAA	TCA	GCT	TTG	GTT	ACC	ATC	GTA	GGA	AAG	GGA	TTT	ATA	AAT	GCT		1
113																	
Ser	Gln	Ser	Ala	Leu	Val	Thr	Ile	Val	Gly	Lys	Gly	Phe	Ile	Asn	Ala		
310				315						320					325		
ACC	AAT	TCA	AGT	GAA	GAT	TAT	GAA	ATT	GAC	CAA	TAT	GAA	GAG	TTT	TGT		1
161																	
Thr	Asn	Ser	Ser	Glu	Asp	Tyr	Glu	Ile	Asp	Gln	Tyr	Glu	Glu	Phe	Cys		
				330					335					340			
TTT	TCT	GTC	AGG	TTT	AAA	GCC	TAC	CCA	CAA	ATC	AGA	TGT	ACG	TGG	ACC		1
209																	
Phe	Ser	Val	Arg	Phe	Lys	Ala	Tyr	Pro	Gln	Ile	Arg	Cys	Thr	Trp	Thr		
			345					350					355				
TTC	TCT	CGA	AAA	TCA	TTT	CCT	TGT	GAG	CAA	AAG	GGT	CTT	GAT	AAC	GGA		1
257																	

SeqListing.txt

Phe	Ser	Arg	Lys	Ser	Phe	Pro	Cys	Glu	Gln	Lys	Gly	Leu	Asp	Asn	Gly		
		360					365					370					
TAC	AGC	ATA	TCC	AAG	TTT	TGC	AAT	CAT	AAG	CAC	CAG	CCA	GGA	GAA	TAT		1
305																	
Tyr	Ser	Ile	Ser	Lys	Phe	Cys	Asn	His	Lys	His	Gln	Pro	Gly	Glu	Tyr		
	375					380					385						
ATA	TTC	CAT	GCA	GAA	AAT	GAT	GAT	GCC	CAA	TTT	ACC	AAA	ATG	TTC	ACG		1
353																	
Ile	Phe	His	Ala	Glu	Asn	Asp	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr		
390					395					400					405		
CTG	AAT	ATA	AGA	AGG	AAA	CCT	CAA	GTG	CTC	GCA	GAA	GCA	TCG	GCA	AGT		1
401																	
Leu	Asn	Ile	Arg	Arg	Lys	Pro	Gln	Val	Leu	Ala	Glu	Ala	Ser	Ala	Ser		
				410					415					420			
CAG	GCG	TCC	TGT	TTC	TCG	GAT	GGA	TAC	CCA	TTA	CCA	TCT	TGG	ACC	TGG		1
449																	
Gln	Ala	Ser	Cys	Phe	Ser	Asp	Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp		
			425					430					435				
AAG	AAG	TGT	TCA	GAC	AAG	TCT	CCC	AAC	TGC	ACA	GAA	GAG	ATC	ACA	GAA		1
497																	
Lys	Lys	Cys	Ser	Asp	Lys	Ser	Pro	Asn	Cys	Thr	Glu	Glu	Ile	Thr	Glu		
		440					445					450					
GGA	GTC	TGG	AAT	AGA	AAG	GCT	AAC	AGA	AAA	GTG	TTT	GGA	CAG	TGG	GTG		1
545																	
Gly	Val	Trp	Asn	Arg	Lys	Ala	Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val		
	455					460					465						
TCG	AGC	AGT	ACT	CTA	AAC	ATG	AGT	GAA	GCC	ATA	AAA	GGG	TTC	CTG	GTC		1
593																	
Ser	Ser	Ser	Thr	Leu	Asn	Met	Ser	Glu	Ala	Ile	Lys	Gly	Phe	Leu	Val		
470					475					480					485		
AAG	TGC	TGT	GCA	TAC	AAT	TCC	CTT	GGC	ACA	TCT	TGT	GAG	ACG	ATC	CTT		1
641																	
Lys	Cys	Cys	Ala	Tyr	Asn	Ser	Leu	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Leu		
				490					495					500			
TTA	AAC	TCT	CCA	GGC	CCC	TTC	CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCA	TTC		1
689																	
Leu	Asn	Ser	Pro	Gly	Pro	Phe	Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe		
			505					510					515				

SeqListing.txt

TAT	GCA	ACA	ATT	GGT	GTT	TGT	CTC	CTC	TTC	ATT	GTC	GTT	TTA	ACC	CTG	1
737																
Tyr	Ala	Thr	Ile	Gly	Val	Cys	Leu	Leu	Phe	Ile	Val	Val	Leu	Thr	Leu	
		520					525					530				
CTA	ATT	TGT	CAC	AAG	TAC	AAA	AAG	CAA	TTT	AGG	TAT	GAA	AGC	CAG	CTA	1
785																
Leu	Ile	Cys	His	Lys	Tyr	Lys	Lys	Gln	Phe	Arg	Tyr	Glu	Ser	Gln	Leu	
	535					540					545					
CAG	ATG	GTA	CAG	GTG	ACC	GGC	TCC	TCA	GAT	AAT	GAG	TAC	TTC	TAC	GTT	1
833																
Gln	Met	Val	Gln	Val	Thr	Gly	Ser	Ser	Asp	Asn	Glu	Tyr	Phe	Tyr	Val	
550					555					560					565	
GAT	TTC	AGA	GAA	TAT	GAA	TAT	GAT	CTC	AAA	TGG	GAG	TTT	CCA	AGA	GAA	1
881																
Asp	Phe	Arg	Glu	Tyr	Glu	Tyr	Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	Glu	
			570						575					580		
AAT	TTA	GAG	TTT	GGG	AAG	GTA	CTA	GGA	TCA	GGT	GCT	TTT	GGA	AAA	GTG	1
929																
Asn	Leu	Glu	Phe	Gly	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Lys	Val	
			585					590					595			
ATG	AAC	GCA	ACA	GCT	TAT	GGA	ATT	AGC	AAA	ACA	GGA	GTC	TCA	ATC	CAG	1
977																
Met	Asn	Ala	Thr	Ala	Tyr	Gly	Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln	
		600					605					610				
GTT	GCC	GTC	AAA	ATG	CTG	AAA	GAA	AAA	GCA	GAC	AGC	TCT	GAA	AGA	GAG	2
025																
Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Lys	Ala	Asp	Ser	Ser	Glu	Arg	Glu	
	615					620					625					
GCA	CTC	ATG	TCA	GAA	CTC	AAG	ATG	ATG	ACC	CAG	CTG	GGA	AGC	CAC	GAG	2
073																
Ala	Leu	Met	Ser	Glu	Leu	Lys	Met	Met	Thr	Gln	Leu	Gly	Ser	His	Glu	
630					635					640					645	
AAT	ATT	GTG	AAC	CTG	CTG	GGG	GCG	TGC	ACA	CTG	TCA	GGA	CCA	ATT	TAC	2
121																
Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Leu	Ser	Gly	Pro	Ile	Tyr	
			650						655					660		
TTG	ATT	TTT	GAA	TAC	TGT	TGC	TAT	GGT	GAT	CTT	CTC	AAC	TAT	CTA	AGA	2
169																
Leu	Ile	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	

SeqListing.txt

	665	670	675	
AGT AAA AGA GAA AAA TTT CAC AGG ACT TGG ACA GAG ATT TTC AAG GAA 217				2
Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu 680 685 690				
CAC AAT TTC AGT TTT TAC CCC ACT TTC CAA TCA CAT CCA AAT TCC AGC 265				2
His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser 695 700 705				
ATG CCT GGT TCA AGA GAA GTT CAG ATA CAC CCG GAC TCG GAT CAA ATC 313				2
Met Pro Gly Ser Arg Glu Val Gln Ile His Pro Asp Ser Asp Gln Ile 710 715 720 725				
TCA GGG CTT CAT GGG AAT TCA TTT CAC TCT GAA GAT GAA ATT GAA TAT 361				2
Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr 730 735 740				
GAA AAC CAA AAA AGG CTG GAA GAA GAG GAG GAC TTG AAT GTG CTT ACA 409				2
Glu Asn Gln Lys Arg Leu Glu Glu Glu Glu Asp Leu Asn Val Leu Thr 745 750 755				
TTT GAA GAT CTT CTT TGC TTT GCA TAT CAA GTT GCC AAA GGA ATG GAA 457				2
Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu 760 765 770				
TTT CTG GAA TTT AAG TCG TGT GTT CAC AGA GAC CTG GCC GCC AGG AAC 505				2
Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn 775 780 785				
GTG CTT GTC ACC CAC GGG AAA GTG GTG AAG ATA TGT GAC TTT GGA TTG 553				2
Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu 790 795 800 805				
GCT CGA GAT ATC ATG AGT GAT TCC AAC TAT GTT GTC AGG GGC AAT GCC 601				2
Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala 810 815 820				
CGT CTG CCT GTA AAA TGG ATG GCC CCC GAA AGC CTG TTT GAA GGC ATC				2

SeqListing.txt

649	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	
				825					830					835			
TAC	ACC	ATT	AAG	AGT	GAT	GTC	TGG	TCA	TAT	GGA	ATA	TTA	CTG	TGG	GAA		2
697																	
Tyr	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu		
		840					845					850					
ATC	TTC	TCA	CTT	GGT	GTG	AAT	CCT	TAC	CCT	GGC	ATT	CCG	GTT	GAT	GCT		2
745																	
Ile	Phe	Ser	Leu	Gly	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala		
	855					860					865						
AAC	TTC	TAC	AAA	CTG	ATT	CAA	AAT	GGA	TTT	AAA	ATG	GAT	CAG	CCA	TTT		2
793																	
Asn	Phe	Tyr	Lys	Leu	Ile	Gln	Asn	Gly	Phe	Lys	Met	Asp	Gln	Pro	Phe		
870					875					880					885		
TAT	GCT	ACA	GAA	GAA	ATA	TAC	ATT	ATA	ATG	CAA	TCC	TGC	TGG	GCT	TTT		2
841																	
Tyr	Ala	Thr	Glu	Glu	Ile	Tyr	Ile	Ile	Met	Gln	Ser	Cys	Trp	Ala	Phe		
				890					895					900			
GAC	TCA	AGG	AAA	CGG	CCA	TCC	TTC	CCT	AAT	TTG	ACT	TCG	TTT	TTA	GGA		2
889																	
Asp	Ser	Arg	Lys	Arg	Pro	Ser	Phe	Pro	Asn	Leu	Thr	Ser	Phe	Leu	Gly		
			905					910					915				
TGT	CAG	CTG	GCA	GAT	GCA	GAA	GAA	GCG	ATG	TAT	CAG	AAT	GTG	GAT	GGC		2
937																	
Cys	Gln	Leu	Ala	Asp	Ala	Glu	Glu	Ala	Met	Tyr	Gln	Asn	Val	Asp	Gly		
		920					925					930					
CGT	GTT	TCG	GAA	TGT	CCT	CAC	ACC	TAC	CAA	AAC	AGG	CGA	CCT	TTC	AGC		2
985																	
Arg	Val	Ser	Glu	Cys	Pro	His	Thr	Tyr	Gln	Asn	Arg	Arg	Pro	Phe	Ser		
	935					940					945						
AGA	GAG	ATG	GAT	TTG	GGG	CTA	CTC	TCT	CCG	CAG	GCT	CAG	GTC	GAA	GAT		3
033																	
Arg	Glu	Met	Asp	Leu	Gly	Leu	Leu	Ser	Pro	Gln	Ala	Gln	Val	Glu	Asp		
950					955					960					965		
TCG	TAGAGGAACA	ATTTAGTTTT	AAGGACTTCA	TCCCTCCACC	TATCCCTAAC												3
086																	
Ser																	

SeqListing.txt

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AGGCTGTAGA TTACCAAAAC AAGATTAATT TCATCACTAA AAGAAAATCT ATTATCAACT 3
146

GCTGCTTCAC CAGACTTTTC TCTAGAAGCC GTCTGCGTTT ACTCTTGTTT TCAAAGGGAC 3
206

TTTTGTAAAA TCAAATCATC CTGTCACAAG GCAGGAGGAG CTGATAATGA ACTTTATTGG 3
266

AGCATTGATC TGCATCCAAG GCCTTCTCAG GCCGGCTTGA GTGAATTGTG TACCTGAAGT 3
326

ACAGTATATT CTTGTAAATA CATAAAACAA AAGCATTTTG CTAAGGAGAA GCTAATATGA 3
386

TTTTTTAAGT CTATGTTTTA AAATAATATG TAAATTTTTC AGCTATTTAG TGATATATTT 3
446

TATGGGTGGG AATAAAATTT CTACTACAGA AAAAAAAAAA AAAAAAAAAA AAAAA 3
501

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met  Pro  Ala  Leu  Ala  Arg  Asp  Ala  Gly  Thr  Val  Pro  Leu  Leu  Val  Val
-27      -25              -20              -15

Phe  Ser  Ala  Met  Ile  Phe  Gly  Thr  Ile  Thr  Asn  Gln  Asp  Leu  Pro  Val
      -10              -5              1              5

Ile  Lys  Cys  Val  Leu  Ile  Asn  His  Lys  Asn  Asn  Asp  Ser  Ser  Val  Gly
              10              15              20

Lys  Ser  Ser  Ser  Tyr  Pro  Met  Val  Ser  Glu  Ser  Pro  Glu  Asp  Leu  Gly
              25              30              35

Cys  Ala  Leu  Arg  Pro  Gln  Ser  Ser  Gly  Thr  Val  Tyr  Glu  Ala  Ala  Ala
      40              45              50

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SeqListing.txt

Val	Glu	Val	Asp	Val	Ser	Ala	Ser	Ile	Thr	Leu	Gln	Val	Leu	Val	Asp	55	60	65
Ala	Pro	Gly	Asn	Ile	Ser	Cys	Leu	Trp	Val	Phe	Lys	His	Ser	Ser	Leu	70	75	80
Asn	Cys	Gln	Pro	His	Phe	Asp	Leu	Gln	Asn	Arg	Gly	Val	Val	Ser	Met	90	95	100
Val	Ile	Leu	Lys	Met	Thr	Glu	Thr	Gln	Ala	Gly	Glu	Tyr	Leu	Leu	Phe	105	110	115
Ile	Gln	Ser	Glu	Ala	Thr	Asn	Tyr	Thr	Ile	Leu	Phe	Thr	Val	Ser	Ile	120	125	130
Arg	Asn	Thr	Leu	Leu	Tyr	Thr	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys	Met	135	140	145
Glu	Asn	Gln	Asp	Ala	Leu	Val	Cys	Ile	Ser	Glu	Ser	Val	Pro	Glu	Pro	150	155	160
Ile	Val	Glu	Trp	Val	Leu	Cys	Asp	Ser	Gln	Gly	Glu	Ser	Cys	Lys	Glu	170	175	180
Glu	Ser	Pro	Ala	Val	Val	Lys	Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu	185	190	195
Phe	Gly	Thr	Asp	Ile	Arg	Cys	Cys	Ala	Arg	Asn	Glu	Leu	Gly	Arg	Glu	200	205	210
Cys	Thr	Arg	Leu	Phe	Thr	Ile	Asp	Leu	Asn	Gln	Thr	Pro	Gln	Thr	Thr	215	220	225
Leu	Pro	Gln	Leu	Phe	Leu	Lys	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys	230	235	240
Lys	Ala	Val	His	Val	Asn	His	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu	250	255	260
Asn	Lys	Ala	Leu	Glu	Glu	Gly	Asn	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser	265	270	275
Thr	Asn	Arg	Thr	Met	Ile	Arg	Ile	Leu	Phe	Ala	Phe	Val	Ser	Ser	Val	280	285	290
Ala	Arg	Asn	Asp	Thr	Gly	Tyr	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro	295	300	305

SeqListing.txt

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Ser Gln Ser Ala Leu Val Thr Ile Val Gly Lys Gly Phe Ile Asn Ala
310                               315                 320                 325

Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
                               330                 335                 340

Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
                               345                 350                 355

Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
                               360                 365                 370

Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
                               375                 380                 385

Ile Phe His Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr
390                               395                 400                 405

Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
                               410                 415                 420

Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
                               425                 430                 435

Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
                               440                 445                 450

Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
                               455                 460                 465

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
470                               475                 480                 485

Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
                               490                 495                 500

Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe
                               505                 510                 515

Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu
                               520                 525                 530

Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu
                               535                 540                 545

Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val
550                               555                 560                 565

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SeqListing.txt

Asp	Phe	Arg	Glu	Tyr	Glu	Tyr	Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	Glu	570	575	580
Asn	Leu	Glu	Phe	Gly	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Lys	Val	585	590	595
Met	Asn	Ala	Thr	Ala	Tyr	Gly	Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln	600	605	610
Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Lys	Ala	Asp	Ser	Ser	Glu	Arg	Glu	615	620	625
Ala	Leu	Met	Ser	Glu	Leu	Lys	Met	Met	Thr	Gln	Leu	Gly	Ser	His	Glu	630	635	640
Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Leu	Ser	Gly	Pro	Ile	Tyr	650	655	660
Leu	Ile	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	665	670	675
Ser	Lys	Arg	Glu	Lys	Phe	His	Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	Glu	680	685	690
His	Asn	Phe	Ser	Phe	Tyr	Pro	Thr	Phe	Gln	Ser	His	Pro	Asn	Ser	Ser	695	700	705
Met	Pro	Gly	Ser	Arg	Glu	Val	Gln	Ile	His	Pro	Asp	Ser	Asp	Gln	Ile	710	715	720
Ser	Gly	Leu	His	Gly	Asn	Ser	Phe	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	730	735	740
Glu	Asn	Gln	Lys	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	745	750	755
Phe	Glu	Asp	Leu	Leu	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	760	765	770
Phe	Leu	Glu	Phe	Lys	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	775	780	785
Val	Leu	Val	Thr	His	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	790	795	800
Ala	Arg	Asp	Ile	Met	Ser	Asp	Ser	Asn	Tyr	Val	Val	Arg	Gly	Asn	Ala	810	815	820

SeqListing.txt

Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	825	830	835	
Tyr	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	840	845	850	
Ile	Phe	Ser	Leu	Gly	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala	855	860	865	
Asn	Phe	Tyr	Lys	Leu	Ile	Gln	Asn	Gly	Phe	Lys	Met	Asp	Gln	Pro	Phe	870	875	880	885
Tyr	Ala	Thr	Glu	Glu	Ile	Tyr	Ile	Ile	Met	Gln	Ser	Cys	Trp	Ala	Phe	890	895	900	
Asp	Ser	Arg	Lys	Arg	Pro	Ser	Phe	Pro	Asn	Leu	Thr	Ser	Phe	Leu	Gly	905	910	915	
Cys	Gln	Leu	Ala	Asp	Ala	Glu	Glu	Ala	Met	Tyr	Gln	Asn	Val	Asp	Gly	920	925	930	
Arg	Val	Ser	Glu	Cys	Pro	His	Thr	Tyr	Gln	Asn	Arg	Arg	Pro	Phe	Ser	935	940	945	
Arg	Glu	Met	Asp	Leu	Gly	Leu	Leu	Ser	Pro	Gln	Ala	Gln	Val	Glu	Asp	950	955	960	965
Ser																			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

SeqListing.txt

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 208..4311

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 265..4308

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 208..264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTGTCCCG CAGCCGGATA ACCTGGCTGA CCCGATTCCG CGGACACCCG TGCAGCCGCG
60

GCTGGAGCCA GGGCGCCGGT GCCCGCGCTC TCCCCGGTCT TGCCTGCGG GGGCCGATAC
120

CGCCTCTGTG ACTTCTTTGC GGGCCAGGGA CGGAGAAGGA GTCTGTGCCT GAGAACTGG
180

GCTCTGTGCC CAGGCGCGAG GTGCAGG ATG GAG AGC AAG GGC CTG CTA GCT
231

Met Glu Ser Lys Gly Leu Leu Ala
-19 -15

GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC GCC TCT GTG GGT TTG
279

Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala Ser Val Gly Leu
-10 -5 1 5

CCT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC ACA CAG AAA GAC ATA
327

Pro Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr Gln Lys Asp Ile
10 15 20

CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT ACT TGC AGG GGA CAG
375

Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr Cys Arg Gly Gln
25 30 35

CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG CGT GAT TCT GAG GAA
423

Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg Asp Ser Glu Glu

SeqListing.txt

40	45	50
AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC AGT ATC TTC TGC AAA 471	Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp Ser Ile Phe Cys Lys 55 60 65	
ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT ACT GGA GCC TAC AAG 519	Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr Gly Ala Tyr Lys 70 75 80 85	
TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT GTT TAT GTC TAT GTT 567	Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val Tyr Val Tyr Val 90 95 100	
CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC AGT GAC CAG CAT GGC 615	Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp Gln His Gly 105 110 115	
ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT GTG GTG ATC CCC TGC 663	Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val Val Ile Pro Cys 120 125 130	
CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT TGC GCT AGG TAT CCA 711	Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys Ala Arg Tyr Pro 135 140 145	
GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT TCC TGG GAC AGC GAG 759	Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp Asp Ser Glu 150 155 160 165	
ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC TAT GCC GGC ATG GTC 807	Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser Tyr Ala Gly Met Val 170 175 180	
TTC TGT GAG GCA AAG ATC AAT GAT GAA ACC TAT CAG TCT ATC ATG TAC 855	Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr Gln Ser Ile Met Tyr 185 190 195	
ATA GTT GTG GTT GTA GGA TAT AGG ATT TAT GAT GTG ATT CTG AGC CCC		

SeqListing.txt

903	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	Val	Ile	Leu	Ser	Pro	
			200					205					210				
CCG	CAT	GAA	ATT	GAG	CTA	TCT	GCC	GGA	GAA	AAA	CTT	GTC	TTA	AAT	TGT		
951	Pro	His	Glu	Ile	Glu	Leu	Ser	Ala	Gly	Glu	Lys	Leu	Val	Leu	Asn	Cys	
		215					220					225					
ACA	GCG	AGA	ACA	GAG	CTC	AAT	GTG	GGG	CTT	GAT	TTC	ACC	TGG	CAC	TCT		
999	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Leu	Asp	Phe	Thr	Trp	His	Ser	
		230				235					240					245	
CCA	CCT	TCA	AAG	TCT	CAT	CAT	AAG	AAG	ATT	GTA	AAC	CGG	GAT	GTG	AAA		1
047	Pro	Pro	Ser	Lys	Ser	His	His	Lys	Lys	Ile	Val	Asn	Arg	Asp	Val	Lys	
				250						255					260		
CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	AGC	ACC	TTG	ACA	ATA		1
095	Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	Ser	Thr	Leu	Thr	Ile	
			265						270					275			
GAA	AGT	GTG	ACC	AAG	AGT	GAC	CAA	GGG	GAA	TAC	ACC	TGT	GTA	GCG	TCC		1
143	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln	Gly	Glu	Tyr	Thr	Cys	Val	Ala	Ser	
			280					285					290				
AGT	GGA	CGG	ATG	ATC	AAG	AGA	AAT	AGA	ACA	TTT	GTC	CGA	GTT	CAC	ACA		1
191	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn	Arg	Thr	Phe	Val	Arg	Val	His	Thr	
		295					300					305					
AAG	CCT	TTT	ATT	GCT	TTC	GGT	AGT	GGG	ATG	AAA	TCT	TTG	GTG	GAA	GCC		1
239	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser	Gly	Met	Lys	Ser	Leu	Val	Glu	Ala	
					315						320				325		
ACA	GTG	GGC	AGT	CAA	GTC	CGA	ATC	CCT	GTG	AAG	TAT	CTC	AGT	TAC	CCA		1
287	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile	Pro	Val	Lys	Tyr	Leu	Ser	Tyr	Pro	
				330					335					340			
GCT	CCT	GAT	ATC	AAA	TGG	TAC	AGA	AAT	GGA	AGG	CCC	ATT	GAG	TCC	AAC		1
335	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg	Asn	Gly	Arg	Pro	Ile	Glu	Ser	Asn	
			345						350					355			

SeqListing.txt

TAC 383	ACA	ATG	ATT	GTT	GGC	GAT	GAA	CTC	ACC	ATC	ATG	GAA	GTG	ACT	GAA	1
Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu	Leu	Thr	Ile	Met	Glu	Val	Thr	Glu	
		360					365					370				
AGA 431	GAT	GCA	GGA	AAC	TAC	ACG	GTC	ATC	CTC	ACC	AAC	CCC	ATT	TCA	ATG	1
Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val	Ile	Leu	Thr	Asn	Pro	Ile	Ser	Met	
	375					380					385					
GAG 479	AAA	CAG	AGC	CAC	ATG	GTC	TCT	CTG	GTT	GTG	AAT	GTC	CCA	CCC	CAG	1
Glu	Lys	Gln	Ser	His	Met	Val	Ser	Leu	Val	Val	Asn	Val	Pro	Pro	Gln	
390					395					400					405	
ATC 527	GGT	GAG	AAA	GCC	TTG	ATC	TCG	CCT	ATG	GAT	TCC	TAC	CAG	TAT	GGG	1
Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser	Pro	Met	Asp	Ser	Tyr	Gln	Tyr	Gly	
				410					415					420		
ACC 575	ATG	CAG	ACA	TTG	ACA	TGC	ACA	GTC	TAC	GCC	AAC	CCT	CCC	CTG	CAC	1
Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	Ala	Asn	Pro	Pro	Leu	His	
			425					430					435			
CAC 623	ATC	CAG	TGG	TAC	TGG	CAG	CTA	GAA	GAA	GCC	TGC	TCC	TAC	AGA	CCC	1
His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	Ala	Cys	Ser	Tyr	Arg	Pro	
		440					445					450				
GGC 671	CAA	ACA	AGC	CCG	TAT	GCT	TGT	AAA	GAA	TGG	AGA	CAC	GTG	GAG	GAT	1
Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	Lys	Glu	Trp	Arg	His	Val	Glu	Asp	
	455					460					465					
TTC 719	CAG	GGG	GGA	AAC	AAG	ATC	GAA	GTC	ACC	AAA	AAC	CAA	TAT	GCC	CTG	1
Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	Val	Thr	Lys	Asn	Gln	Tyr	Ala	Leu	
470					475					480					485	
ATT 767	GAA	GGA	AAA	AAC	AAA	ACT	GTA	AGT	ACG	CTG	GTC	ATC	CAA	GCT	GCC	1
Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	
				490					495					500		
AAC 815	GTG	TCA	GCG	TTG	TAC	AAA	TGT	GAA	GCC	ATC	AAC	AAA	GCG	GGA	CGA	1

SeqListing.txt

Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	Glu	Ala	Ile	Asn	Lys	Ala	Gly	Arg	
			505					510					515			
GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	GGT	CCT	GAA	ATT	ACT	1
863																
Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	Gly	Pro	Glu	Ile	Thr	
		520					525					530				
GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	AGT	GTG	TCC	CTG	TTG	1
911																
Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Leu	
	535					540					545					
TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	ACG	TGG	TAC	AAG	CTT	1
959																
Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	
550					555					560					565	
GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	TCA	CTC	ACA	CCA	GTT	2
007																
Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	Ser	Leu	Thr	Pro	Val	
				570					575					580		
TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	GGC	ACC	ATG	TTT	TCT	2
055																
Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	Gly	Thr	Met	Phe	Ser	
			585					590					595			
AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	CAG	AAT	GCC	TCT	CTG	2
103																
Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	Gln	Asn	Ala	Ser	Leu	
		600					605					610				
CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	GAT	AAG	AAG	ACC	AAG	2
151																
Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	Asp	Lys	Lys	Thr	Lys	
	615					620					625					
AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	CTA	GAG	CGC	ATG	GCA	2
199																
Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	Leu	Glu	Arg	Met	Ala	
630					635					640					645	
CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	ACA	ACC	ATT	GGC	GAG	2
247																
Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	Thr	Thr	Ile	Gly	Glu	
				650					655					660		

SeqListing.txt

ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	CCT	ACC	CCA	CAC	ATT	2
295																
Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	Pro	Thr	Pro	His	Ile	
			665					670					675			
ACA	TGG	TTC	AAA	GAC	AAC	GAG	ACC	CTG	GTA	GAA	GAT	TCA	GGC	ATT	GTA	2
343																
Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	
		680					685					690				
CTG	AGA	GAT	GGG	AAC	CGG	AAC	CTG	ACT	ATC	CGC	AGG	GTG	AGG	AAG	GAG	2
391																
Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	
	695					700					705					
GAT	GGA	GGC	CTC	TAC	ACC	TGC	CAG	GCC	TGC	AAT	GTC	CTT	GGC	TGT	GCA	2
439																
Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Cys	Asn	Val	Leu	Gly	Cys	Ala	
710					715					720					725	
AGA	GCG	GAG	ACG	CTC	TTC	ATA	ATA	GAA	GGT	GCC	CAG	GAA	AAG	ACC	AAC	2
487																
Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	
				730					735					740		
TTG	GAA	GTC	ATT	ATC	CTC	GTC	GGC	ACT	GCA	GTG	ATT	GCC	ATG	TTC	TTC	2
535																
Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	Thr	Ala	Val	Ile	Ala	Met	Phe	Phe	
			745				750						755			
TGG	CTC	CTT	CTT	GTC	ATT	CTC	GTA	CGG	ACC	GTT	AAG	CGG	GCC	AAT	GAA	2
583																
Trp	Leu	Leu	Leu	Val	Ile	Leu	Val	Arg	Thr	Val	Lys	Arg	Ala	Asn	Glu	
		760					765					770				
GGG	GAA	CTG	AAG	ACA	GGC	TAC	TTG	TCT	ATT	GTC	ATG	GAT	CCA	GAT	GAA	2
631																
Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Val	Met	Asp	Pro	Asp	Glu	
	775					780					785					
TTG	CCC	TTG	GAT	GAG	CGC	TGT	GAA	CGC	TTG	CCT	TAT	GAT	GCC	AGC	AAG	2
679																
Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu	Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	
790					795					800					805	
TGG	GAA	TTC	CCC	AGG	GAC	CGG	CTG	AAA	CTA	GGA	AAA	CCT	CTT	GGC	CGC	2
727																
Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	

SeqListing.txt

810										815			820					
GGT	GCC	TTC	GGC	CAA	GTG	ATT	GAG	GCA	GAC	GCT	TTT	GGA	ATT	GAC	AAG	2		
775																		
Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys			
			825					830					835					
ACA	GCG	ACT	TGC	AAA	ACA	GTA	GCC	GTC	AAG	ATG	TTG	AAA	GAA	GGA	GCA	2		
823																		
Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Gly	Ala			
		840					845					850						
ACA	CAC	AGC	GAG	CAT	CGA	GCC	CTC	ATG	TCT	GAA	CTC	AAG	ATC	CTC	ATC	2		
871																		
Thr	His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile			
	855					860					865							
CAC	ATT	GGT	CAC	CAT	CTC	AAT	GTG	GTG	AAC	CTC	CTA	GGC	GCC	TGC	ACC	2		
919																		
His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr			
870					875				880						885			
AAG	CCG	GGA	GGG	CCT	CTC	ATG	GTG	ATT	GTG	GAA	TTC	TCG	AAG	TTT	GGA	2		
967																		
Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	Phe	Ser	Lys	Phe	Gly			
				890					895					900				
AAC	CTA	TCA	ACT	TAC	TTA	CGG	GGC	AAG	AGA	AAT	GAA	TTT	GTT	CCC	TAT	3		
015																		
Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr			
			905					910					915					
AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	GAC	TAC	GTT	GGG	GAG	3		
063																		
Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	Asp	Tyr	Val	Gly	Glu			
		920					925					930						
CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	ATC	ACC	AGC	AGC	CAG	3		
111																		
Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	Ile	Thr	Ser	Ser	Gln			
		935				940					945							
AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	TCG	CTC	AGT	GAT	GTA	3		
159																		
Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	Ser	Leu	Ser	Asp	Val			
950					955					960					965			
GAG	GAA	GAA	GAA	GCT	TCT	GAA	GAA	CTG	TAC	AAG	GAC	TTC	CTG	ACC	TTG	3		

SeqListing.txt

207
Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe Leu Thr Leu
970 975 980

GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC 3
255
Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe
985 990 995

TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG GCA GCA CGA AAC ATT 3
303
Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile
1000 1005 1010

CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT GAC TTC GGC TTG GCC 3
351
Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala
1015 1020 1025

CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA AAA GGA GAT GCC CGA 3
399
Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg
1030 1035 1040 1045

CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT TTT GAC AGA GTA TAC 3
447
Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr
1050 1055 1060

ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG TTG CTC TGG GAA ATA 3
495
Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
1065 1070 1075

TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC AAG ATT GAT GAA GAA 3
543
Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu
1080 1085 1090

TTT TGT AGG AGA TTG AAA GAA GGA ACT AGA ATG CGG GCT CCT GAC TAC 3
591
Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr
1095 1100 1105

ACT ACC CCA GAA ATG TAC CAG ACC ATG CTG GAC TGC TGG CAT GAG GAC 3
639
Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Glu Asp
1110 1115 1120 1125

SeqListing.txt

CCC AAC CAG AGA CCC TCG TTT TCA GAG TTG GTG GAG CAT TTG GGA AAC 687	3
Pro Asn Gln Arg Pro Ser Phe Ser Glu Leu Val Glu His Leu Gly Asn 1130 1135 1140	
CTC CTG CAA GCA AAT GCG CAG CAG GAT GGC AAA GAC TAT ATT GTT CTT 735	3
Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu 1145 1150 1155	
CCA ATG TCA GAG ACA CTG AGC ATG GAA GAG GAT TCT GGA CTC TCC CTG 783	3
Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser Leu 1160 1165 1170	
CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG GAA GTG TGC GAC CCC 831	3
Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu Val Cys Asp Pro 1175 1180 1185	
AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAT TAT CTC CAG AAC 879	3
Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser His Tyr Leu Gln Asn 1190 1195 1200 1205	
AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA ACA TTT GAA GAT ATC 927	3
Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile 1210 1215 1220	
CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA GAT GAC AGC CAG ACA 975	3
Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Ser Gln Thr 1225 1230 1235	
GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG AAA ACT CTG GAA GAC 023	4
Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp 1240 1245 1250	
AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG ATG CCC AGT AAA AGC 071	4
Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met Met Pro Ser Lys Ser 1255 1260 1265	
AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG ACC AGT GGC TAC CAG 119	4

SeqListing.txt

Arg	Glu	Ser	Val	Ala	Ser	Glu	Gly	Ser	Asn	Gln	Thr	Ser	Gly	Tyr	Gln	
1270					1275					1280					1285	
TCT	GGG	TAT	CAC	TCA	GAT	GAC	ACA	GAC	ACC	ACC	GTG	TAC	TCC	AGC	GAC	4
167																
Ser	Gly	Tyr	His	Ser	Asp	Asp	Thr	Asp	Thr	Thr	Val	Tyr	Ser	Ser	Asp	
				1290					1295					1300		
GAG	GCA	GGA	CTT	TTA	AAG	ATG	GTG	GAT	GCT	GCA	GTT	CAC	GCT	GAC	TCA	4
215																
Glu	Ala	Gly	Leu	Leu	Lys	Met	Val	Asp	Ala	Ala	Val	His	Ala	Asp	Ser	
			1305					1310					1315			
GGG	ACC	ACA	CTG	CAG	CTC	ACC	TCC	TGT	TTA	AAT	GGA	AGT	GGT	CCT	GTC	4
263																
Gly	Thr	Thr	Leu	Gln	Leu	Thr	Ser	Cys	Leu	Asn	Gly	Ser	Gly	Pro	Val	
		1320					1325					1330				
CCG	GCT	CCG	CCC	CCA	ACT	CCT	GGA	AAT	CAC	GAG	AGA	GGT	GCT	GCT	TAGATTTTCA	
4318																
Pro	Ala	Pro	Pro	Pro	Thr	Pro	Gly	Asn	His	Glu	Arg	Gly	Ala	Ala		
	1335					1340					1345					
AGTGTGTGTTT	TTTCCACCAC	CCGGAAGTAG	CCACATTGTA	TTTTTCATTTT	TGGAGGAGGG											4
378																
ACCTCAGACT	GCAAGGAGCT	TGTCCTCAGG	GCATTTCCAG	AGAAGATGCC	CATGACCCAA											4
438																
GAATGTGTTG	ACTCTACTCT	CTTTTCCATT	CATTTAAAAG	TCCTATATAA	TGTGCCCTGC											4
498																
TGTGGTCTCA	CTACCAGTTA	AAGCAAAAGA	CTTTCAAACA	CGTGGACTCT	GTCCTCCAAG											4
558																
AAGTGGCAAC	GGCACCTCTG	TGAAACTGGA	TCGAATGGGC	AATGCTTTGT	GTGTTGAGGA											4
618																
TGGGTGAGAT	GTCCCAGGGC	CGAGTCTGTC	TACCTTGGAG	GCTTTGTGGA	GGATGCGGCT											4
678																
ATGAGCCAAG	TGTTAAGTGT	GGGATGTGGA	CTGGGAGGAA	GGAAGGCGCA	AGCCGTCCGG											4
738																
AGAGCGGTTG	GAGCCTGCAG	ATGCATTGTG	CTGGCTCTGG	TGGAGGTGGG	CTTGTGGCCT											4
798																
GTCAGGAAAC	GCAAAGGCGG	CCGGCAGGGT	TTGGTTTTGG	AAGGTTTGCG	TGCTCTTCAC											4

SeqListing.txt

858

AGTCGGGTTA CAGGCGAGTT CCCTGTGGCG TTCCTACTC CTAATGAGAG TTCCTTCCGG 918	4
ACTCTTACGT GTCTCCTGGC CTGGCCCCAG GAAGGAAATG ATGCAGCTTG CTCCTTCCTC 978	4
ATCTCTCAGG CTGTGCCTTA ATTCAGAACA CCAAAAGAGA GGAACGTCGG CAGAGGCTCC 038	5
TGACGGGGCC GAAGAATTGT GAGAACAGAA CAGAAACTCA GGGTTTCTGC TGGGTGGAGA 098	5
CCCACGTGGC GCCCTGGTGG CAGGTCTGAG GGTTCCTGT CAAGTGGCGG TAAAGGCTCA 158	5
GGCTGGTGTT CTTCTCTAT CTCCACTCCT GTCAGGCCCC CAAGTCCTCA GTATTTTAGC 218	5
TTTGTGGCTT CCTGATGGCA GAAAAATCTT AATTGGTTGG TTTGCTCTCC AGATAATCAC 278	5
TAGCCAGATT TCGAAATTAC TTTTtagccg AGGTTATGAT AACATCTACT GTATCCTTTA 338	5
GAATTTTAAC CTATAAACT ATGTCTACTG GTTTCTGCCT GTGTGCTTAT GTTAAAAAAA 398	5
AAAAAAA 406	5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ser	Lys	Gly	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu
-19				-15					-10					-5	

Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Pro	Gly	Asp	Phe	Leu	His	Pro	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SeqListing.txt

1

5

10

Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr
 15 20 25
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 30 35 40 45
 Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly
 50 55 60
 Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val
 65 70 75
 Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile
 80 85 90
 Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile
 95 100 105
 Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
 110 115 120 125
 Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
 130 135 140
 Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
 145 150 155
 Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
 160 165 170
 Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
 175 180 185
 Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
 190 195 200 205
 Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
 210 215 220
 Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
 225 230 235
 Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
 240 245 250
 Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys

SeqListing.txt

255					260					265					
Met	Phe	Leu	Ser	Thr	Leu	Thr	Ile	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln
270					275					280					285
Gly	Glu	Tyr	Thr	Cys	Val	Ala	Ser	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn
				290					295					300	
Arg	Thr	Phe	Val	Arg	Val	His	Thr	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser
			305					310					315		
Gly	Met	Lys	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile
		320					325					330			
Pro	Val	Lys	Tyr	Leu	Ser	Tyr	Pro	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg
		335				340					345				
Asn	Gly	Arg	Pro	Ile	Glu	Ser	Asn	Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu
350					355					360					365
Leu	Thr	Ile	Met	Glu	Val	Thr	Glu	Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val
				370					375					380	
Ile	Leu	Thr	Asn	Pro	Ile	Ser	Met	Glu	Lys	Gln	Ser	His	Met	Val	Ser
			385					390					395		
Leu	Val	Val	Asn	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser
		400					405					410			
Pro	Met	Asp	Ser	Tyr	Gln	Tyr	Gly	Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr
		415				420					425				
Val	Tyr	Ala	Asn	Pro	Pro	Leu	His	His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu
430					435					440					445
Glu	Glu	Ala	Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys
				450					455					460	
Lys	Glu	Trp	Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu
			465					470					475		
Val	Thr	Lys	Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val
		480					485					490			
Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys
		495				500					505				
Glu	Ala	Ile	Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His

SeqListing.txt

510					515					520					525
Val	Ile	Arg	Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr
				530					535					540	
Glu	Gln	Glu	Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe
			545					550					555		
Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His
		560					565					570			
Met	Gly	Glu	Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp
	575					580					585				
Lys	Leu	Asn	Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile
590					595					600					605
Val	Ala	Phe	Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys
				610					615					620	
Ser	Ala	Gln	Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln
			625					630					635		
Leu	Ile	Ile	Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu
		640					645					650			
Asn	Gln	Thr	Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala
		655				660					665				
Ser	Gly	Asn	Pro	Thr	Pro	His	Ile	Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr
670					675					680					685
Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu
				690					695					700	
Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln
			705					710					715		
Ala	Cys	Asn	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile
		720					725					730			
Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly
	735					740					745				
Thr	Ala	Val	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Leu	Val
750					755					760					765
Arg	Thr	Val	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu

SeqListing.txt

770										775					780				
Ser	Ile	Val	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu				
			785					790					795						
Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu				
		800					805					810							
Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu				
	815					820					825								
Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala				
830					835					840					845				
Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu				
				850					855					860					
Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val				
			865					870					875						
Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val				
		880					885					890							
Ile	Val	Glu	Phe	Ser	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly				
	895					900					905								
Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg				
910					915					920					925				
Gln	Gly	Lys	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg				
				930					935					940					
Leu	Asp	Ser	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val				
			945					950					955						
Glu	Glu	Lys	Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Ser	Glu	Glu				
		960					965					970							
Leu	Tyr	Lys	Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe				
	975					980					985								
Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His				
990					995					1000					1005				
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn	Val	Val				
				1010					1015					1020					
Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp				

SeqListing.txt

1025	1030	1035
Tyr Val Arg Lys Gly Asp Ala	Arg Leu Pro Leu Lys	Trp Met Ala Pro
1040	1045	1050
Glu Thr Ile Phe Asp Arg Val	Tyr Thr Ile Gln Ser Asp Val	Trp Ser
1055	1060	1065
Phe Gly Val Leu Leu Trp Glu	Ile Phe Ser Leu Gly Ala Ser	Pro Tyr
1070	1075	1080
Pro Gly Val Lys Ile Asp Glu	Glu Phe Cys Arg Arg Leu Lys	Glu Gly
1090	1095	1100
Thr Arg Met Arg Ala Pro Asp	Tyr Thr Thr Pro Glu Met Tyr	Gln Thr
1105	1110	1115
Met Leu Asp Cys Trp His Glu	Asp Pro Asn Gln Arg Pro Ser	Phe Ser
1120	1125	1130
Glu Leu Val Glu His Leu Gly	Asn Leu Leu Gln Ala Asn Ala	Gln Gln
1135	1140	1145
Asp Gly Lys Asp Tyr Ile Val	Leu Pro Met Ser Glu Thr Leu	Ser Met
1150	1155	1160
Glu Glu Asp Ser Gly Leu Ser	Leu Pro Thr Ser Pro Val Ser	Cys Met
1170	1175	1180
Glu Glu Glu Glu Val Cys Asp	Pro Lys Phe His Tyr Asp Asn	Thr Ala
1185	1190	1195
Gly Ile Ser His Tyr Leu Gln	Asn Ser Lys Arg Lys Ser Arg	Pro Val
1200	1205	1210
Ser Val Lys Thr Phe Glu Asp	Ile Pro Leu Glu Glu Pro Glu	Val Lys
1215	1220	1225
Val Ile Pro Asp Asp Ser Gln	Thr Asp Ser Gly Met Val Leu	Ala Ser
1230	1235	1240
Glu Glu Leu Lys Thr Leu Glu	Asp Arg Asn Lys Leu Ser Pro	Ser Phe
1250	1255	1260
Gly Gly Met Met Pro Ser Lys	Ser Arg Glu Ser Val Ala Ser	Glu Gly
1265	1270	1275
Ser Asn Gln Thr Ser Gly Tyr	Gln Ser Gly Tyr His Ser Asp	Asp Thr

SeqListing.txt

1280		1285		1290
Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val				
1295		1300		1305
Asp Ala Ala Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser				
1310		1315		1320
				1325
Cys Leu Asn Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly				
	1330		1335	1340
Asn His Glu Arg Gly Ala Ala				
1345				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTCGTCGACT TTCTGTCACCAT GAGTGCACTTCT GATCCTAGCCCT TGTGGGAGCTGC
60
TGTTGCTGACTA CAAAGATGATGA TGACAAGATCTA
96

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

SeqListing.txt

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCTTAGATCTT GTCATCATCATC TTTGTAGTCAGC AACAGCAGCTCC CACAAGGGCTAG 6
0

GATCAGAAGTGC ACTCATGGTGAC AGAAAGTCGACG 9
6

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAAGATC TCAAACCAAG ACCTGCCTGT
30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAATGGCGGC CGCTCAGGAGA TGTTGTCTTGGA

34

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Tyr Lys Asp Asp Asp Asp Lys Ile

1

5